

Amendments to Specification

Please replace the following paragraphs:

Paragraph beginning on page 12, line 10

SEQ ID NO:47 is the nucleotide sequence comprising the sugarbeet cDNA insert in clone ~~sugarbeet1~~sugarbeet2, encoding an almost entire sugarbeet isoflavone synthase.

Paragraph beginning on page 13, line 3

SEQ ID NO:60 is the ~~amino acid~~nucleotide sequence comprising the sugarbeet cDNA insert in clone ~~sugarbeet2~~sugarbeet1, encoding an almost entire sugarbeet isoflavone synthase.

Paragraph beginning on page 39, line 15

Amplification was carried out in two steps. The first amplification reaction was performed using 1 µL of first strand cDNA and primer set one (SEQ ID NO:11 and SEQ ID NO:12) with 30 cycles of 94°C for 30 seconds, 50°C for 30 seconds and 72°C for one minute. A second amplification reaction was done with 1 µL of the resulting product with primer set two (SEQ ID NO:13 and SEQ ID NO:14) and using 30 cycles of 94°C for 30 seconds, 50.5°C for 30 seconds and 72°C for one minute. The resulting PCR sequence was cloned into pCR2.1 using TOPO™ TA Cloning Kit (Invitrogen). Plasmid DNA was purified using QIAFilter cartridges (Qiagen Inc) or Wizard Plus Minipreps DNA Purification System (Promega) following the manufacturer's instructions. Sequence was generated on an ABI Automatic sequencer using dye terminator technology and using a combination of vector and insert-specific primers. Sequence editing was performed using DNASTar (DNASTAR, Inc.). All sequences represent coverage at least two times in both directions. The nucleotide sequence comprising the cDNA insert in clone ~~sugarbeet1~~sugarbeet 2 is shown in SEQ ID NO:47; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:48. The nucleotide sequence comprising the cDNA insert in clone ~~sugarbeet2~~sugarbeet 1 is shown in SEQ ID NO:60[[61]]; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:61.

Paragraph beginning on page 41, line 13:

A consensus sequence was determined by aligning the amino acid sequences of the present invention using the Clustal method of alignment and this sequence is shown in SEQ ID NO:66. Amino acids not conserved are indicated by Xaa. These are:

Xaa ₁₀	Phe or Leu
Xaa ₁₆	Ser or Leu
Xaa ₂₃	Ser or Thr
Xaa ₂₅	Ile or Lys
Xaa ₃₉	Lys or Arg
Xaa ₄₈	Pro or Leu
Xaa ₆₀	Pro or Leu
Xaa ₇₃	Leu or His
Xaa ₇₄	Ser or Tyr
Xaa ₉₅	Ala or Thr
Xaa ₉₆	Asn or His
Xaa ₁₀₂	Asn or Ser
Xaa ₁₁₀	Ile, Val, or Thr
Xaa ₁₁₂	Arg or His
Xaa ₁₁₇	Asn or Ser
Xaa ₁₁₈	Ser or Leu
Xaa ₁₂₁	Met or Arg
Xaa ₁₂₂	Ala or Val
Xaa ₁₂₄	Phe or Ile
Xaa ₁₂₉	Lys or Arg
Xaa ₁₄₇	Lys or Glu
Xaa ₁₅₉	Leu or Phe
Xaa ₁₆₂	Ala or Val
Xaa ₁₆₆	Ser or Gly
Xaa ₁₇₀	Gln or Arg
Xaa ₁₇₅	Val or Leu
Xaa ₁₈₃	Ala or Thr
Xaa ₁₈₇	Thr or Ile

Xaa ₁₉₁	Met or Val
Xaa ₂₀₉	Phe or Tyr
Xaa ₂₁₉	Arg or Trp
Xaa ₂₂₃	Tyr or His
Xaa ₂₅₃	Gly or Glu
Xaa ₂₅₉	Lys or Glu
Xaa ₂₆₃	Val or Asp
Xaa ₂₆₄	Val, Asp, or Ile
Xaa ₂₆₈	Ala or Val
Xaa ₂₇₂	Phe or Leu
Xaa ₂₈₅	Thr or Met
Xaa₂₉₃	Glu or Asp
<u>Xaa₂₉₂</u>	<u>Any amino acid</u>
<u>Xaa₂₉₃</u>	<u>Any amino acid</u>
Xaa ₂₉₄	Thr, or Ile
Xaa ₃₀₁	Phe or Leu
Xaa ₃₀₆	Thr or Ile
Xaa ₃₁₁	Val or Glu
Xaa ₃₁₂	Val or Ala
Xaa ₃₂₅	Arg or Lys
Xaa ₃₂₈	Gln or Glu
<u>Xaa₃₂₉</u>	<u>Any amino acid</u>
Xaa ₃₃₄	Val or Ala
Xaa ₃₄₂	Arg or Ile
Xaa ₃₇₇	Thr or Ile
Xaa ₃₈₁	Glu or Gly
Xaa ₃₈₅	Tyr, His, or Cys
Xaa ₃₈₇	Ile or Thr
Xaa ₃₉₃	Val or Ile
Xaa ₃₉₄	Leu or Pro
Xaa ₄₀₂	Arg or Lys
Xaa ₄₀₄	Ser or Pro
Xaa ₄₁₃	Ser or Phe

Xaa ₄₂₂	Glu or Gly
Xaa ₄₂₈	Gly or Arg
Xaa ₄₂₉	Pro or Leu
Xaa ₄₃₅	Gln or Arg
Xaa ₄₄₇	Arg or Gly
Xaa ₄₅₃	Asn, Ser, or Ile
Xaa ₄₅₉	Met or Thr, and
Xaa ₄₈₅	Asp or Gly

Please replace the sequence listing with the enclosed amended sequence listing.